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SPM

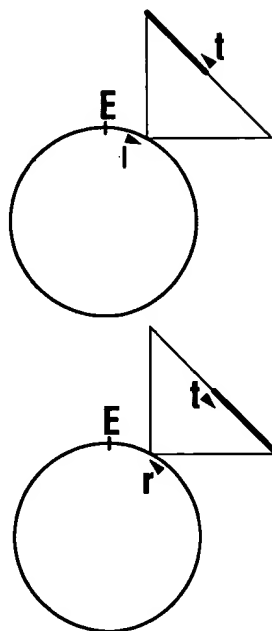


FIGURE 1A



FIGURE 1B

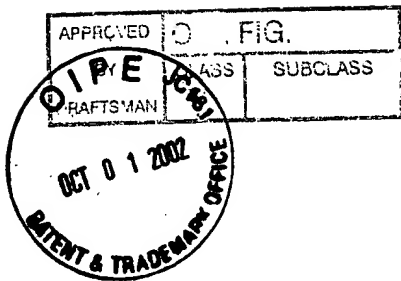
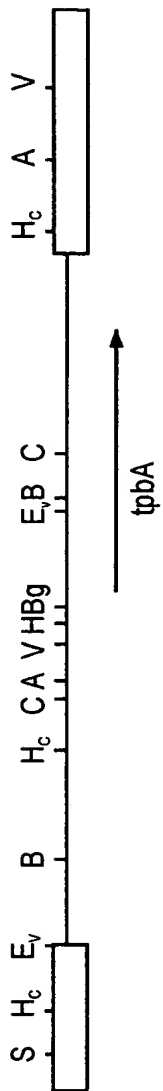
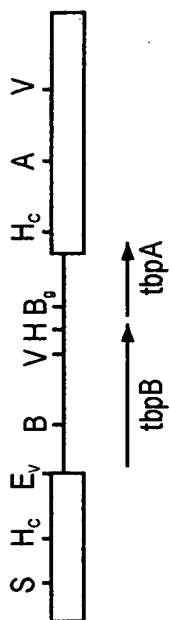


FIGURE 2

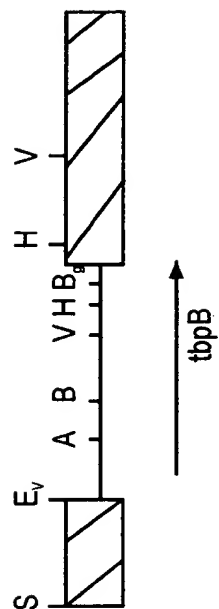
Plasmid 9



Plasmid 10



Plasmid 482



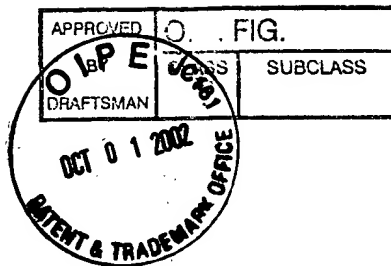


FIGURE 3A

tbpB

	10	20	30	40	50
1	CGCTTGCAGA	TTTGTAAAAA	ATTTAGCTAA	AATCAGACCT	GGCTTGTATT
51	TTAGGGTTAT	TATGGAACAG	ACAACGGAAC	AAATAGATTA	TAAATTATTA
101	AAGCATCGTT	TTCGTGGCTA	TTTACCGCTT	GTGATTGATG	TGGAACAGAG
151	GCTTAAATGC	CCAAACTGTG	CCTTATTGGA	ATTGGCCGGA	ATTACTTTAA
201	AATTGGACGA	GCCAAGGTTA	TCTTATTGCC	GGATTCAACA	ATGCCAATTT
251	CCAATTTGCG	GCCATTGGAG	GGGGCGATTT	TCAAGGGCCG	AATATTTACC
301	CTCAGTCATT	AAAATTCAAC	GGCATTCATA	TTCACAACCC	TCTAGAGGAA
351	GCGGTTTAGA	GAATATTGCC	CAATTCCCGG	AAATGTTCAA	AATGGTTCGC
401	AAAGCAATGA	AGGAAGCAAG	GCTGCCAACG	GGCGGTGATT	GTTGCCCCAC
451	AATGCCAGCG	TTCGATCAGG	GCTTTTTTAC	AGGGCTGCGA	TTAAACGGAA
501	TGCCAAGCGA	GAGATCCCTT	TCACCCTTTT	GGCGATGTTT	GACTACCGCC
551	GCCACCCTTT	GCAGGTTTTA	TGTTATGGGC	AAACCGTGTT	CGTTAAAAGC
601	CTGCCAGTGC	AAAATCCGTT	CACGTAGCAG	CACTATAGGG	CGAATTGGGT
651	ACCGGGCCCC	CCTCGAGGTC	GACGGTATCG	ATAAAGCTTC	ATATCGAATT
701	CCTGCAGCCC	GGGGGATCCG	ATGCGCCTTG	CGGCTCAAGT	TATTAGTGGC
751	ATCGGTTTTT	TGGGTGATGG	TGTCATTTTG	CATAAGAAAA	ATGATGCGAT
801	TTCAGGTTTA	CCCACTGCGG	CGATTATTTG	GGCTTCTGCG	GGGATCGGTA
851	TTGCTGCAGG	GGAGGGTTTC	GTGTTTCATG	CGGTCATCGC	CACTGTCATT
901	ATTTTGGTGT	CTATTCGATT	ATGTCCGTTG	GTTCAACGTT	GGGTTCATCG
951	TAAATCACAA	CGTCGTCGAC	GAAATATTCT	TGTCAATGAT	GCGGAAAGCA
1001	TACGGAAAGT	TACCCAATTG	TTATTCAATA	ATCAGTATCG	TATTGAACAT
1051	ATACAAGTCA	AAGATCAAAG	TAGTGGAGAA	GTTGCCGGTT	ACAAATTCGT

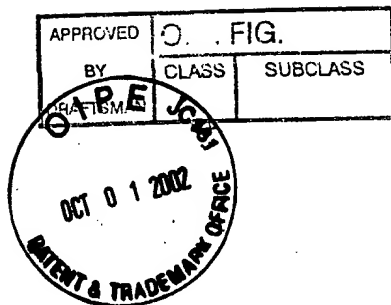


FIGURE 3B

1101 ATTGATTCCA CAATGTTCAA AGATGCGTAT GCTTTACTTA AAGCAGAAGA
1151 TGGCGAATAC TGTTC AAGTA GATATCATGA AAAAGAGTGC TTATATTCAA
1201 TTTTTTATTT TTTATTTAAT TTCTTTCCAC AAAAGATCAT TTTCAATTAT
1251 ATATACTGGA ATTTTGCCTT ACGCTATCTG TCATTTATTA TGCTATTCAA
1301 GCACAACAAA CTATGGAACA ACAATCAAAA TGTACGCTTA TCGGCTGCCG
1351 ATGATTTTGA TAATGATCGA TGTGCAGAAA TATTTGAACT TACGATTTTC
1401 ACTGAGCAGT CAAAGCACGT TCGCGAGTAT CGACTCTACT TTATTTATCG
1451 TTTGTGCACT ATGTATAATC CACCTAATTC CGTGCCTTGG CCATAAAAGC
1501 CCCCTTCAAA TTGTATTTAT ATCAGCTACC GTGCCACCAT TCGTACTTTT
1551 CGGATCAAGA TTAAACAGA ATCCCTGCAT GCACAGCGAA ATCAGCTGCG
1601 GTATGCGAAA CGCCGCAGGA GCGCAGTACG CGAAGTGTAC CGTCACTATC
1651 AGTGCTAGAT TTGTCAATAA AAAATTAGTG ACCAAGCTTG GGTGCATAAT
1701 GATGGTGATG AAAGAACGCT CAATGCTTGA CACGTTGCAG GCTATCTGTA
1751 AGGGTATGGT AGTTACAGGC ACAGCCCAAA CGGCCAATTG CTGGTTTTTT
1801 ATCCTTGATC CGAACAGTAC GAATGGTGGT CACGGTAGTG CATATACATA
1851 CTCAATTGAA GGGGGCTTTT ATGGCCCTAA GGCGACGGAA TTAGGTGGTA
1901 TTGTACATAG TGCAGAAACG GATAAAGATA GAGTCAGTAT TACATTGGC
1951 GGAAAACGTC AAATAGAAAA ATAATCATAA TTCCCCTTTG CTGGTTGTAG
2001 ATAGCAGCGG GCAATTTTTT ATAAAAATTT GCAAAATTTA AATAA

APPROVED	O. FIG.	
BY	CLASS	SUBCLASS

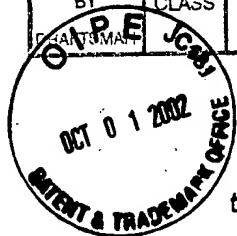


FIGURE 3C

tbpA

	10	20	30	40	50
1	AGACCCTATC	TAATGATAAT	GAAATATCAT	CATTTTCGCT	ATTCACCTGT
51	TGCCTTAACA	GTGTTATTG	CTCTTCTCA	TTCATACGGT	GCTGCGACTG
101	AAAATAAAAA	AATCGAAGAA	AATAACGATC	TAGCTGTTCT	GGATGAAGTT
151	ATTGTGACAG	AGAGCCATTA	TGCTCACGAA	CGTCAAAACG	AAGTAACTGG
201	CTTGGGGAAA	GTAGTGAAAA	ATTATCACGA	AATGAGTAAA	AATCAAATTC
251	TTGGTATTCG	TGATTTAACT	CGCTATGACC	CTGGTATTTT	GGTGGTGGAA
301	CAAGGTCGCG	GTGCAAGTAG	TGGCTATGCC	ATTCGAGGTG	TAGATAAAAA
351	CCGTGTCAGC	TTACTTGTTG	ATGGGCTACC	ACCAGCGCAC	AGTTATCATA
401	CGCTGGTTCA	GATGCTAATG	GTGGTGCAAT	TAATGAGATT	GAGTATGAAA
451	ACATTCGTTT	AATTGAGTTA	AGCAAAGGAG	CAAGTTCTGC	GGAAATATGGC
501	TCTGGTGCGC	ATGGTGGTGC	TATTGGTTTT	CGTACTAAAG	ATCGCCAGGA
551	TATTATTAAA	GAGGGGCAGC	ATTGGGGCTT	ACATAGTAAG	ACCTCTTATG
601	CCAGCAAAAA	TAGCCATTTT	TACAGTCTAT	CGCAGCGGCT	GGTCAGGCGG
651	GTGGTTTTCA	AGCACTTGTT	ATTGCAACTC	ACCGACACGG	TAAAGAGACC
701	AAAATTCATT	CCGAGGCAAA	TCAATTACAT	ATTATTCGGC	GTATAACCGG
751	CTTTCAAAAT	CGCTACGACT	TTACCCAATT	CCGCACAGAA	TGCCTCCTGG
801	AGGATCTTTT	TTTATTGTGG	AAGATACTTG	CCCAACATTA	GATTGTACTC
851	CTCGTGCAAG	GGTTAAGTTG	AACGCGATAA	TTTCCCAGTC	AGAACATTTT
901	CGAATATACG	CCTGGAAGAG	GCGAAACAGC	TTGAGATTCC	TTATCGCACT
951	GAGCTCTCAG	CCCAAAGAAT	ARACCGGTAA	AGATCGCATT	GCACCAAACC
1001	CTTTAGATTA	CAAGAGTAAT	TCTGTTTTTA	TGAAGTTTGG	CTATCACTTT
1051	ACCTCGTCTC	ATTATCTTGG	CGCATCTCAC	AAGATGATAC	AAAACAACGC
1101	ACGATATCCG	TCATSTGCAA	ACGCCAGCTT	ACTATACAAA	AGACGATATT
1151	TACTTATCAC	TTTGGAACCTA	TGTTTATCAA	GGGGATATTA	TTTAGATGGC
1201	TTAGTGTTCA	AGCCAAGGAT	CCCTTATGGG	TTGCGCATAT	GCCATGTGAA

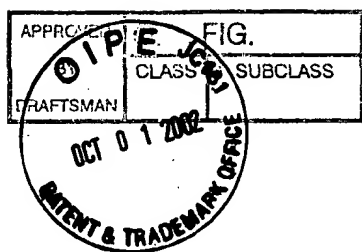


FIGURE 3D

1251 CGTCACCACA AACGTCGTTT AGGATTCACC TATAAATATA AACCAGAGAA
1301 TAATCGCTGG TTGGATAGCA TTAAGTCGTG CGTACGTGCT TTGCGCTCTC
1351 GCTGCTGTGC TCTGAGTAAA CAAGATATTG AACTATATAG CCGGCTACAT
1401 CGCTTGCATT GTAGCGATTA TCCTGTGSTA GATAAAAATT GCGGCCCCGAC
1451 TTTGGATAAA TCTGGTCTAT GTATCGAACT GAGCGTAATA ATTACCAAGA
1501 AAAGCATCGT GTCATTCATT TAGAATTGTA TAAAGCGCTA AATGCTGGTC
1551 AAGGCGTATT TAAGCAAACC CACAACTGA ATTTAGGCTT GGGCTTTGAA
1601 TCGATTAATC GCTTATGATC ATGGGGATAT GACTGCCCAA TATACCAAAG
1651 GCCGGTTATA CCAGCTACCG CGGAGAGGGG CTTTAGATAA TCCATATATT
1701 TATCGCCGCG ATCCACGCAG TATTGAAACG GTATCTTTGT GTAATAATAC
1751 AGCGGCGACA CTTAACTGTG ACGCGTTAAA TAAAGGCATA CGTTTGTACC
1801 TCCGCTGCAC TTAGGAACTA TAGTTTATGA AGGGGATAAT ATTTAGATGG
1851 CTTAGTGTTT AAGCAAGCAA GGATCCCTTA TGGGTGCGC GATATGCCAT
1901 GTGAAGTTTT TGATGAACGT CACCACAAAC GTCGTTTAGG ATTCACACCT
1951 ATAAATATAT AAACCAGAGA ATAATCGCTG GTTGGATAGC ATTAAGTCGT
2001 GCGTACGTGC TTGCGCTCTT CGCTGCTGTG CTGTGAGTTA AACAAGATAT
2051 TGAAACTTAT AGCCGGCTAC ATCGCTTGCA TTGTGAGCGA TTATCCTGTG
2101 GTAGTAGTAA AAATTGCGGC CCGACTTTGG ATAAATCTTG GTCTATGTAT
2151 CGAACTGAGC GTAATAATTA CCAAGAAAAG CATCGTGTCA TTCATTTAGA
2201 ATTTGATAAA GCGCTAAATG CTGGTCAAGG CGTATTTAAG CAAACCCACA
2251 AACTGAATTT AGGATTGGGC TTTGAATCGA TTAATTCGCT TATGGATCAT
2301 GGGGATATGA CTGCCAATA TACCAAAGGC CGGTATATAC AGCTAACCAGC
2351 GAGAGGGCGT TTAGATAATC CATATTTATC GCCGCGATCC ACGCAGTATT
2401 GAAACGGTAT CTTTGTGTAA TAATACACGC GCGACACTAA CTGTGACGCG
2451 TTAAATAAAG GCATACGTTT GTACCTCCGC TGCTGCCTAA TAAATCAAAA
2501 GAATAACCGA GATACGGTTC AGTGTTGTTC CAACCAGTTG CGATGGCCCA

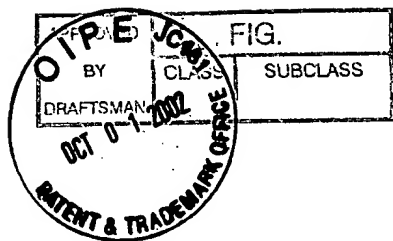


FIGURE 3E

2551 CTACGTGAAC CATCACCTA ATCAAGTTTT TTGGGGTCGA GGTGCCGTAA
2601 AGCACTTAAC CCTTCTGTCG TCTCCCGTGG ATGCTTAAAT TCGCAGCTAG

2651 TGGCAGGCAG GCACGTCCTT CCTCTCGGTG ATTTTCAGGTG CAACTGACCG
2701 GTTCTTGGA CCACCCTTGA TATTAACCGG AGTCAATTAT AAAAACGAGT
2751 TACGTGGAGC GCAATTTATA ATGTCGATGT CAGATACTGT AAAACTCTAT
2801 ATTACCGTGG GCAGCAATTA GGTGACAGGG CCACGGGGCA AGCGAAACCA
2851 GACGGGTACC AATTACACCG ATTTGCCGCC CCCGGGAGAG AAATTTTCAGT
2901 TACCATTCAA AGAAGTTTAG AGCCGGCCAA AAGAAAATAC AAAAAACGCT
2951 GAAAGTATAT TCAGCGCGTT TTTGTTGCTC TAACGGATTA CATACGAATT
3001 CAAAATGTTT TAACGGTCGG TTA

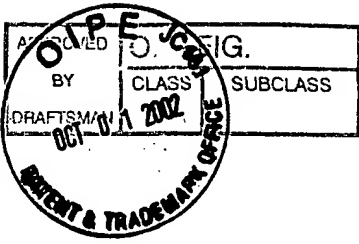


FIGURE 4

CGCTTGCAGATTGTGTAATAAATTAGCTAAATCAGACCTGGCTTGATTTTAGGGTTAATG

-35
-10
MET

PHTBPP

TTTAAAAATAAATAAATAATCCCTTATCATTCCTTTAATTGAATCGGGTTGTTATG

-35
-10
MET

NGTBPP

GTATTGCAGATTGTGTAATAAATAAATAATCCCTTATCATTCCTTTAAT TGAATTGGGTTTATG

-35
-10
MET

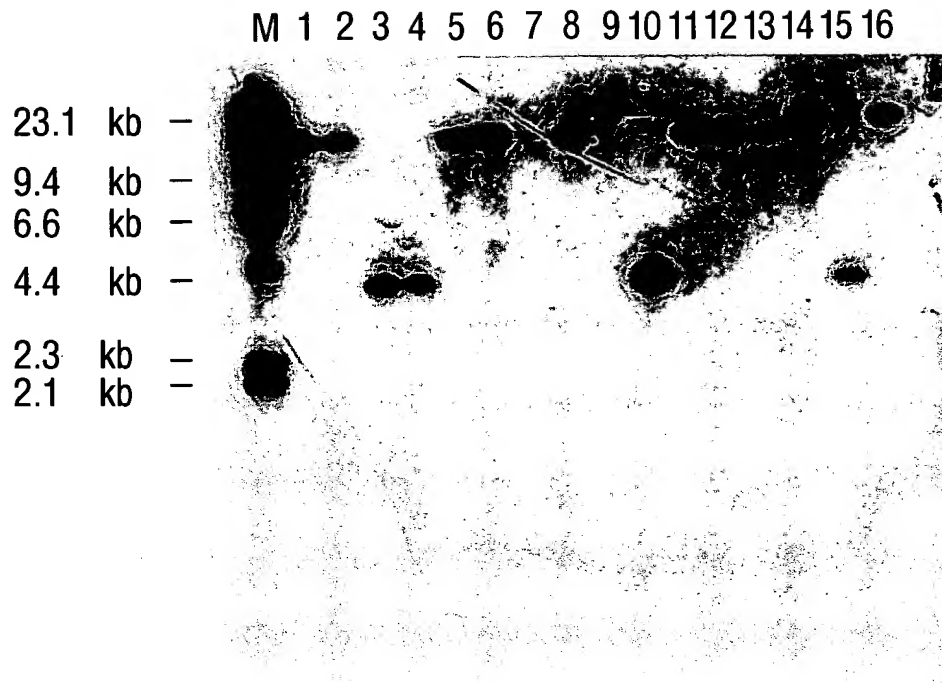
NMTBPP

ADMITTED	FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

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INVENT & TRADEMARK OFFICE

FIGURE 5



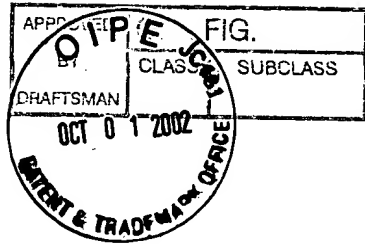
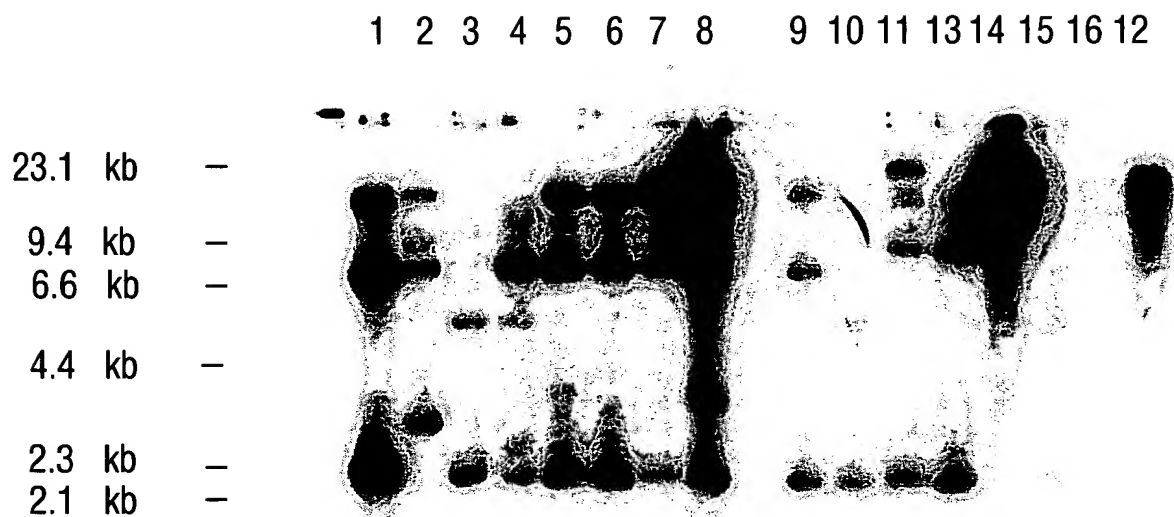


FIGURE 6



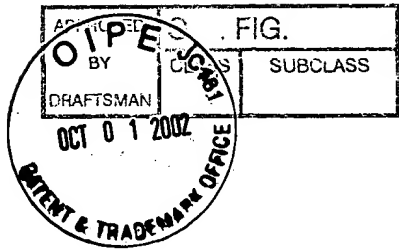


FIGURE 7

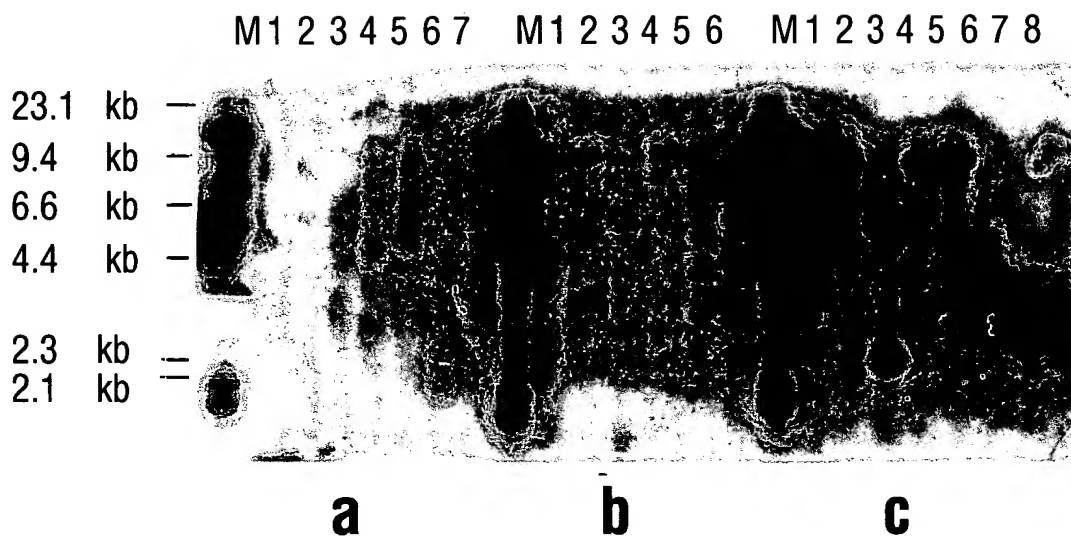
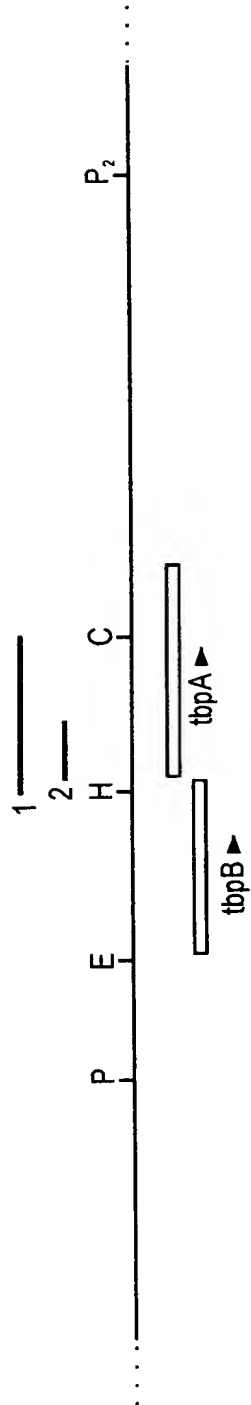
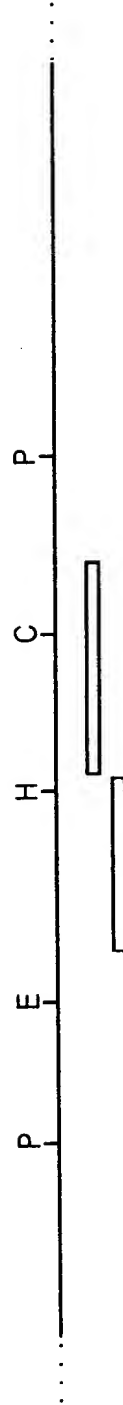


FIGURE 8

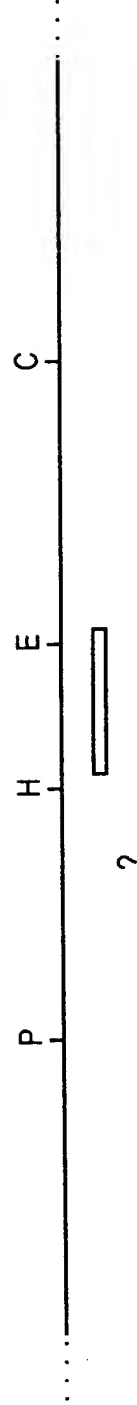
P. haemolytica A1



A. suis 3714



A. pleuropneumoniae CM5, Shope 4074



2kb

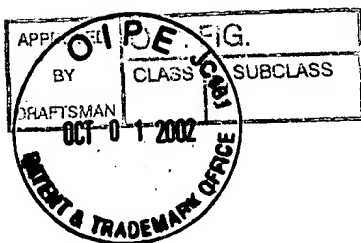


FIGURE 9B

PHTBP	TYKY-KPENNRWLDSINSCVRALRSRCCALSKQDIELYSRLHRLHCS DYP	475
NGTBP1	EYVYTNADKDTWAD----YARL-----SYDRQGIGLDNHFQQTHCSA-D	451
NM1	EYVYHNADKDTWAD----YARL-----SYDRQGIDLDNRLQQTHCSH-D	446
	. * * * * . . . * * * * * * *	
PHTBP	VVDKNCGPTLDKSWSMYRTERNNYQEKHRVHLEFDLALNAGQGVFLQTH	525
NGTBP1	GSDKYCRPSADKPFSYKSDRVIYGESHKLLQAAFKKSFDTAK----IRH	497
NM1	GSDKNCRPDGKNKPYSFYKSDRMIYEESRNLQAVFKKAFDTAK----IRH	492
	* * * * . * . . . * * * * * *	
PHTBP	KLNLGLGFESINSLMDHGDMTAQYTLGRLYQL---PRRDPRSIWTVSLCN	572
NGTBP1	NLSVNLGYDRFGSNLRHQDYQQSAN-RAYSLKTPPQNNGKKTSPNGREK	546
NM1	NLSINLGYDRFKSQLSHSDYYLQNAV-QAYDLITPK---KPPFPNGSKD	537
	. * . . . * * * . * * * * . . . * *	
PHTBP	NT-----RATLNCDAL-NLGIRLYLRCCLINQLNPNRYGSVLFQFGTRV	615
NGTBP1	NPYWVSIGRGNVVRQICLFGNNTYTDCTPRISINGKSYAAV--RDNVRL	594
NM1	NPYRVSIGKTTVNTSPICRFGNNTYTDCTPRNIGGNGYAAV--QDNVRL	585
	* * . * * * . . . * * * . . . * .	
PHTBP	HRTWTPTSLGELPSIRAMAHYVNHHPNQVFWGRGAVKHLT-----LLSS	659
NGTBP1	GR-WADVGAG----LRY--DYRSTHSDDGSVSTGTHRTL SWNAGIVLKPA	637
NM1	GR-WADVGAG----IRY--DYRSTHSEDKSVSTGTHRNLSWNAGVVLKPF	628
	* * . . . * . * . * . * . . . * . * . . . * .	
PHTBP	PWM-LKFAASG--RHVTL SVISG-ATDRFLVPPLILTGVNYKNES---YV	702
NGTBP1	DWLDLT YRTSTGFRLPSFAEMYGWRSGDKIKAVKIDPEKSFNKEAGIVFK	687
NM1	TWMDLT YRASTGFRLPSFAEMYGW RAGESLKTLDLKPEKSFNREAGIVFK	678
	* . * . . * . * . . . * * . .	
PHTBP	SAIYNVDVRYCKTLY-----YRGQQLGDRATGQAKPDGY---QLHRFA	742
NGTBP1	GDFGNLEASWFNNAYRDLIVRGYEAQIKDGKEQVKGNP-AYLNAQSARIT	736
NM1	GDFGNLEASYFNNAYRDLIAFGYETRTQNGQTSASGDP-GYRNAQNARIA	727
	. . . * * . * * * * * . .	
PHTBP	APG-----RNFSYHKKFRPAK---ENTKNAESIFS	770
NGTBP1	GINILGKIDWNGVWDKLPEGWYSTFAYNRVRVRDIKKRADRTDIQSHLFD	786
NM1	GINILGKIDWHGVWGGLPDGLYSTLAYNRIKVKDADIRADRTFVTSYLF	777
 * * *	
PHTBP	A-----FFVGSNGLHTNSKSCFNGLRHEPIPYFFNFLRNVP RFNEYHCCC	815
NGTBP1	AIQPSRYVVGSGYDQPEGKWGVNGMLT-----YSKAKEITELLGSR---	827
NM1	AVQPSRYVLGLGYDHPDGIWGINTMFT-----YSKAKSVDELLGSQ---	818
	* . . * * *	

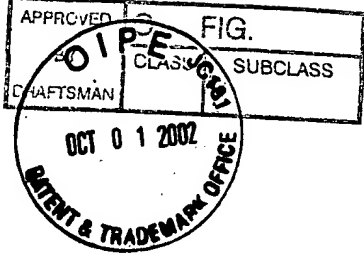


FIGURE 9C

PHTBP	TSLIAASILLHHIYHWVDFRYYYFV--YFCWILHHLIHINSFLMLLSHY	863
NGTBP1	-ALLNGNSRNTKATARRTRPWYIVDVSGYYTVKKHFTLRAGVYNLLNHRY	876
NM1	-ALLNGNANAKKAASRRTRPWYVTDVSGYYNIKKHLTLRAGVYNLLNYRY	867
	. * * * * . * * . *	

PHTBP	--REVVYLTCCACAFNIVTVNGF----CVGCCSNILAEMKF	898
NGTBP1	VTWENVRQTAAGAVNQHKNVGVYNRYAAPGRNYTFSLEMKF	917
NM1	VTWENVRQTAGGAVNQHKNVGVYNRYAAPGRNYTFSLEMKF	908
	. * * * * . . * . . * * * *	

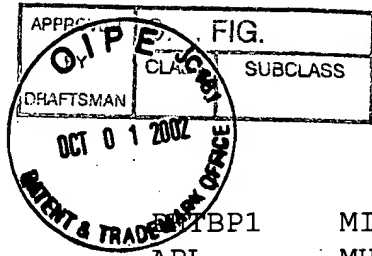


FIGURE 10A

PHTBP1	MIMKYHHFRYSTVALTVLFLALSHSYGAATENKKIEENNDLAVLDEVIVTE	50
APL	MHFKLNPY---ALAFSTLFLVACSGGKGSFD-----LEDVRPNQ	36
APL7	MHFKLNPY---ALAFSTLFLVACSGGKGSFD-----LEDVRPNK	36
	* . * * . * * . *	
PHTBP1	SHYAHERQNEVTGLGKVVKNYHEMSK--NQILG--IRDLTRYDPGISVVE	96
APL	TAKAEKATTSYQDEETKKKTKEELDKLMEPALGYETQILRRNKAPKTETG	86
APL7	TTGVSKEE--YKDVETAKKEKEQLGELMEPALGYVVKV-----PVSSFE	78
 * *	
PHTBP1	QGRGASSGYAIRGVDKNRVSLLDGLPQAHSYHTLSGDANGGAINETI-EY	145
APL	EKRNER---VVELSEDKITKLYQESVEIIPH--LDELNGKTTSNDVYHS	130
APL7	NKK-----VDISD-----IEVITNGNLDDVPYKANSSK-YN	109
 *	
PHTBP1	ENIRSIELSKGASSAEYGSAGHGAIGFRTKDAQ-DIIKEG-----	185
APL	HDSKRLDKNRDLKYVRSGYVYDGSFNEIRNRDNGFHVFKQGIDGYVYYLG	180
APL7	PDIK--TKDSSLQYVRSGYVIDGEHSGSNEK-----GYVYYKG	145
 *	
PHTBP1	----QHWGLDSKTSYASKNSHFLQIAAAGEAGGFALVIATHRH-----	225
APL	VTPSKELPKGKVISYKGTWDFVSNINLEREIDGFDTSBGDKNVSATSITE	230
APL7	NSPAKELPVNQLLTYTGSWDFTSNANLNNE-----EGRPNYLNDDYYTK	189
 *	
PHTBP1	--GKETKI-HSEANKLKHNIIRITGFENRYDFTQIPHRMPPGGSFFIVED	272
APL	TVNRDHKVGEKLGDNVKGVAHSSEFAVDFTDNKKLTGSLYRNG--YINRN	278
APL7	FIGK--RVGLVSGDAKPAKHKYTSQFEVDFATKKMTGKL-----SD	228
 *	
PHTBP1	TCPTLDCTPRARVKLNDRNFPVRTFPEYTPEERNAEQIPYRTEQ--LSAQ	320
APL	KAQEVTKRYSIEADIAGNRFRG-----KAKAEKAGDPIFT-DSNYLEGG	321
APL7	KEKTI---YTVNADIRGNRFTGAATASDKNKGKGESYNFFSADSQSLEGG	275
 *	
PHTBP1	EKTGKDRIAPNPLDYKSNSVFMKFGYHFNSSHYLGAILEDTKQRTISVIC	370
APL	FYGPKAEEMAGKFFTNNKSLFAVFAAKSENGETTTERIIDATKIDLTQFN	371
APL7	FYGPKAEEMAGKFVANDKSLFAVFSAKHNGSNVNTVRIIDASKIDLTNFS	325
	. * *	
PHTBP1	KRQLTI--QKTILTYHLGTMFMKGIIFRWLSVQAKDPLWVAHMPCEVDER	418
APL	AKELNNFGDASVLIIDGQKIDLAGVNFKNKSKTVEINGKTMVAVACCSNLE	421
APL7	ISELNNFGDASVLIIDGKKIKLAGSGFTNKHTIEINGKTMVAVACCSNLE	375
	. * *	

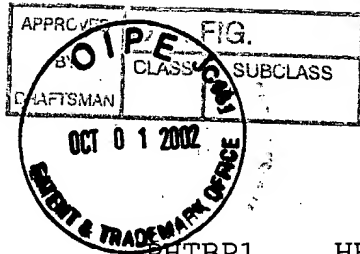


FIGURE 10B

PHTBP1	HHKRRLGFTYKYKPENNRWLDINS CVRALRSRCCALSKQDIELY-----	463
APL	YMK----FGQLWQKEGKQQVKDNSLFLQGERTATDKMPAGGNYKYVGTWD	467
APL7	YMK----FGQLWQQAEGGKPENNSLFLQGERTATDKMPKGGNYKYIGTWD	421
	. * * * . . . *	
PHTBP1	---SRLHRLHCSDYPVVDKNCGPTLDSWSMYRTERNNYQEKATCHSFCI	510
APL	ALVSKGTNWIAEADNNRESGYRTEFDVNFSDKKVNGKLFDKGGVNPVFTV	517
APL7	AQVSKENNWWATADDDRKAGYRTEFDVDFGNKNLSGKLFDKNGVNPVFTV	471
	* * *	
PHTBP1	LKALNAGQGVFKQTHKLNGLGFESNLIRLTIIGIILPNIPKAGYTSYRG	560
APL	DATIN-GNGFIGSAKTSDSGFALDAGSSQHGNVFS DIKVNGGFYGP--T	564
APL7	DAKID-GNGFTGKAKTSDEGFALDSGSSRYENVKFNDVAVSGGFYGP--T	518
	. . * . * * *	
PHTBP1	RGRLDNPYIYRRDPRSIETVSLCNNTRATLLLLRVNKGIRLLLR 604	
APL	AGELGGQFHHKSDNGSVGAV-----FGAKRQIE---K 593	
APL7	AAELGGQFHHKSENGSVGAV-----FGAKQQVK---K 547	
	. * *	

APPROVED	FIG.
BY	CLASS
DATE	SUBCLASS

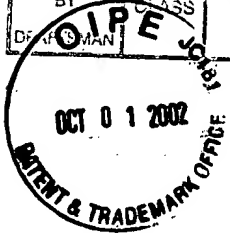


FIGURE 11

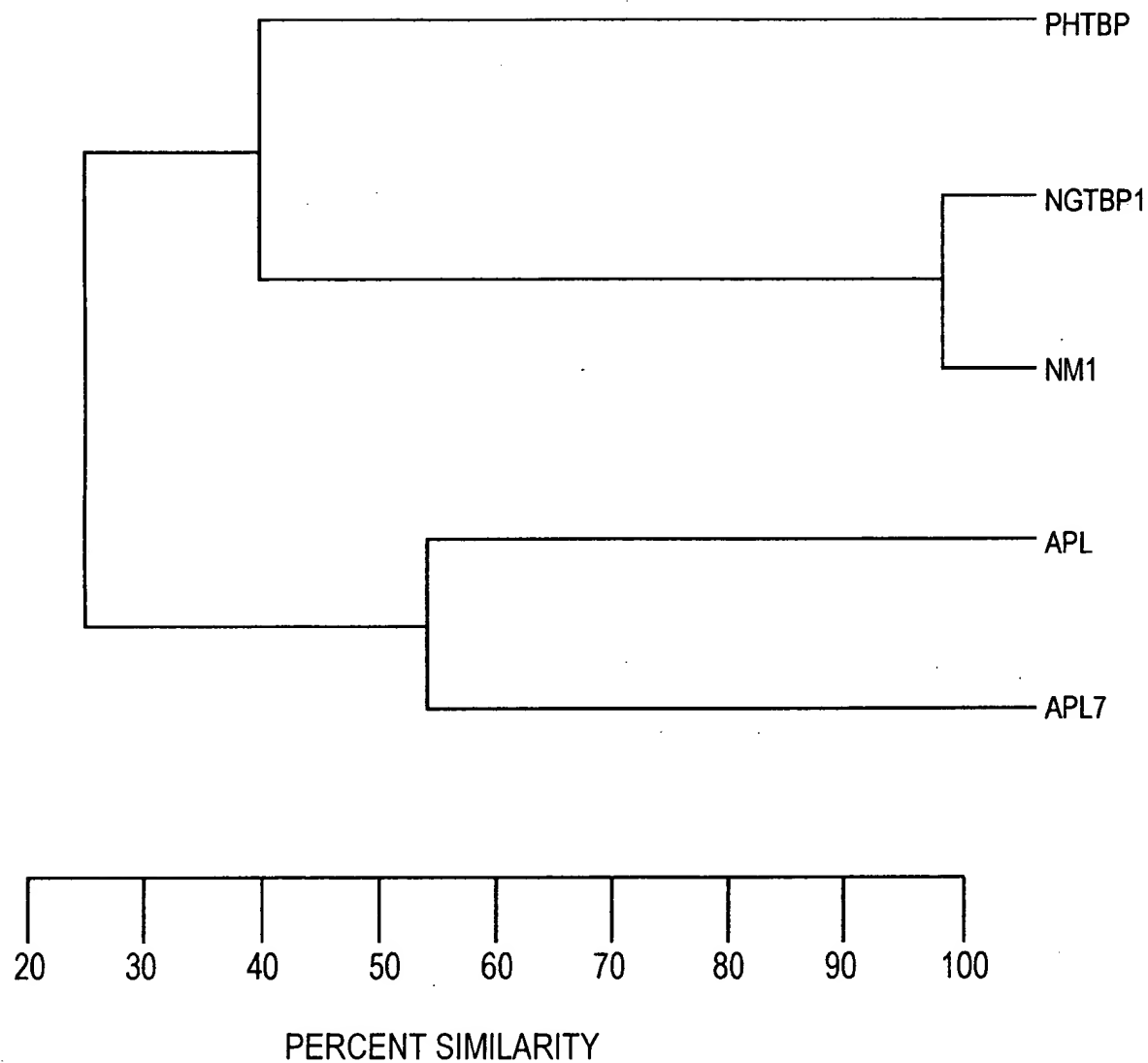


FIGURE 12

1	TonB box	
PHTBP1	DEVIVTE	22
CIRP	ETMVVTA	12
FEPAP	DTIVVTA	17
FHUAP	DTITVTA	13
FECAP	FTLSVDA	30
	. . . *	
2		
PHTBP1	YAIRGVD---KNRVSLLDVG	121
CIRP	VSIRGLDSS---YTLILVDG	105
FEPAP	IDIRGMGPE---NTLILIDG	102
FHUAP	LIIRGFAAEGQSQNNYL-NG	141
FECAP	FGIRGLNPRLTSRSTVLMVG	199
	*** . * *	
3		
PHTBP1	IELSKGASSABYGSGAHGGAIGFRTKD	177
CIRP	IEVVRGPMSSLYGSDALGGVVNIITKK	159
FEPAP	IEVLRGPARARYGNGAAGGVVNIITKK	180
FHUAP	AEIMRGPVSVLYGKSSPGGLLMVSKR	188
FECAP	IDVVRGGGAVRYGPOSVGGVVNFVTRA	251
	. . . * * *	
4		
PHTBP1	FKQTHKLNGLGLF	533
CIRP	PETSESWELGLYY	461
FEPAP	AETSINKEIGLEF	447
FECAP	PSKGKQYEVGVKY	560
FECAP	PEKARTWELGTRY	578
 *	

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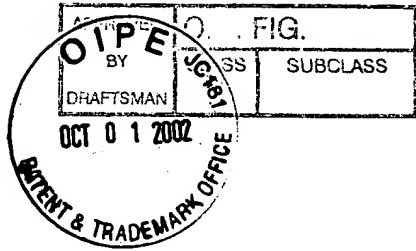
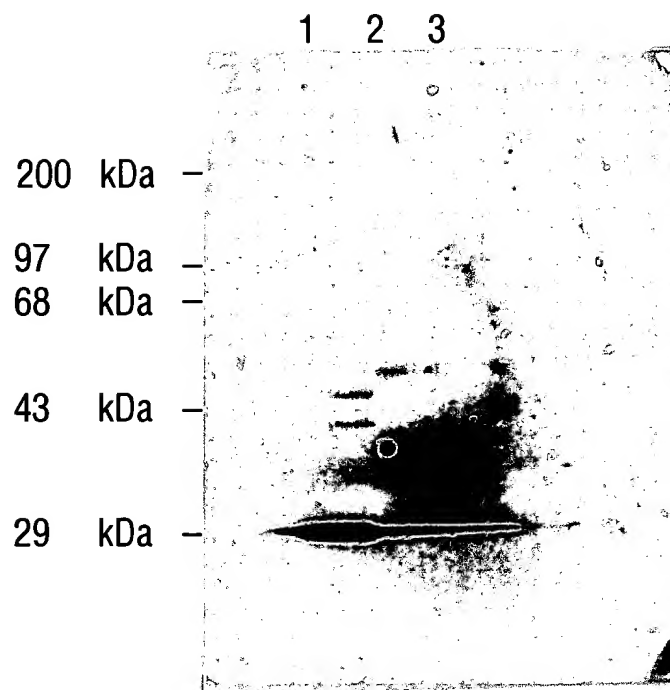


FIGURE 13



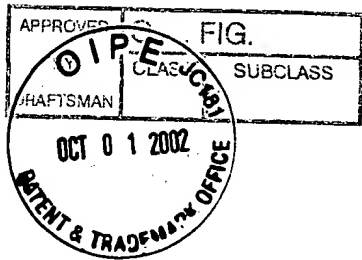
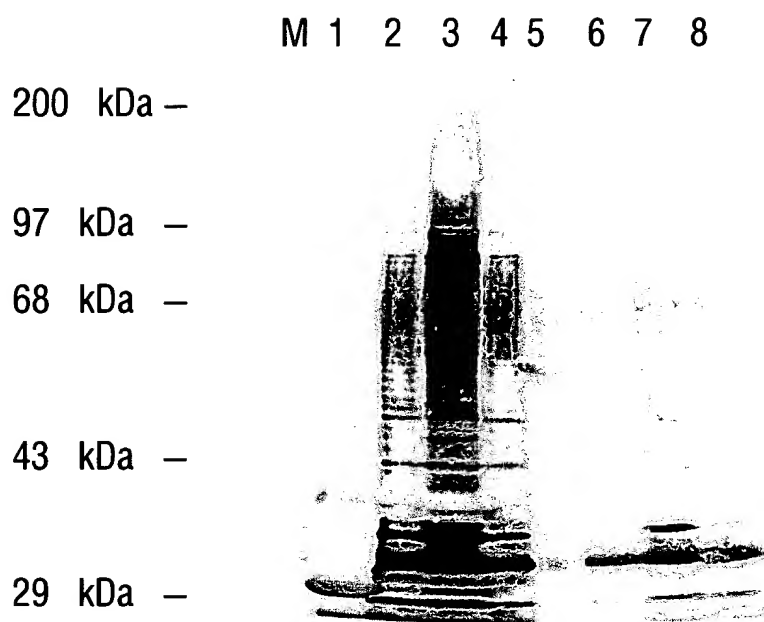


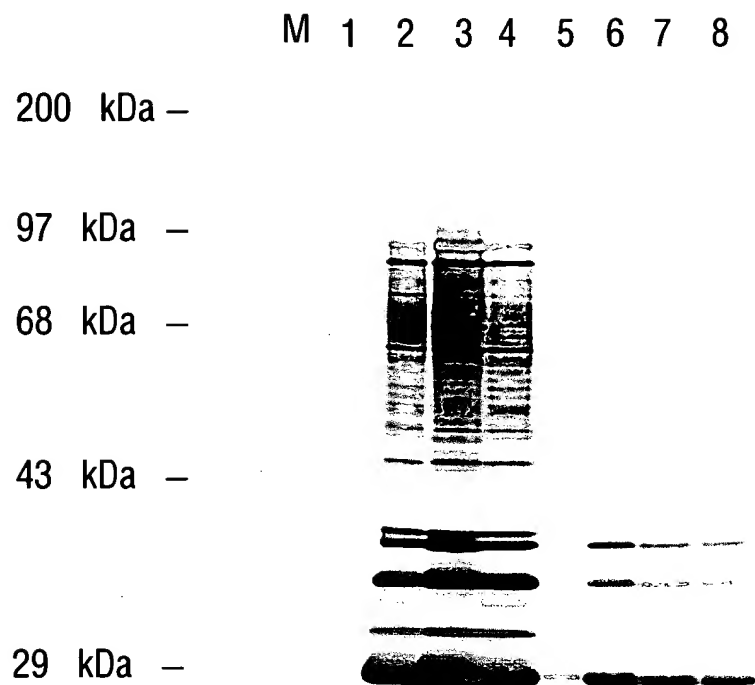
FIGURE 14



APPROVED	FIG.
BY	SUBCLASS
DRAFTSMAN	



FIGURE 15



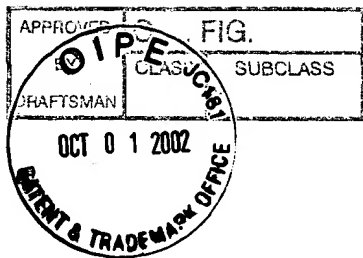


FIGURE 16

	HRP — bTf	HRP — oTf	HRP — cTf	HRP — eTf
h173 —	●	●	●	
h174 —	●	●	●	
h175 —	●	●	●	
h176 —	●	●	●	
h44 —	●	●	●	
h50 —				●

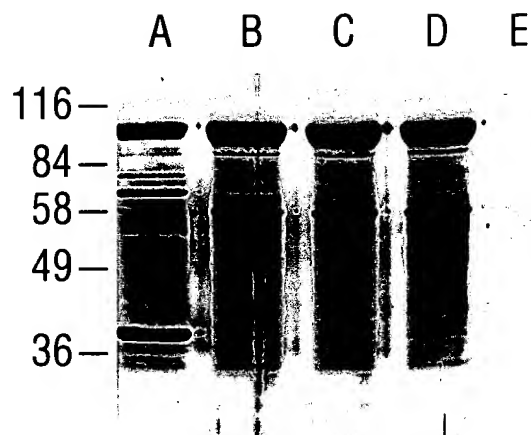
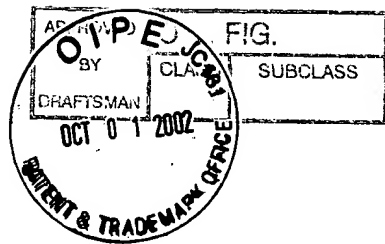


FIGURE 17A

i) h44

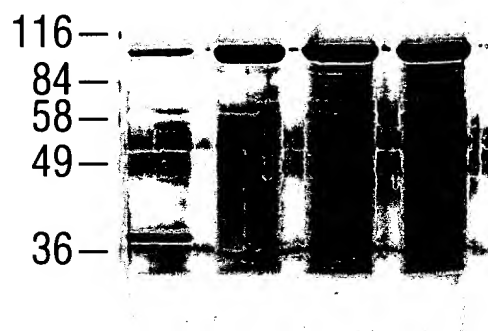


FIGURE 17B

i) h173

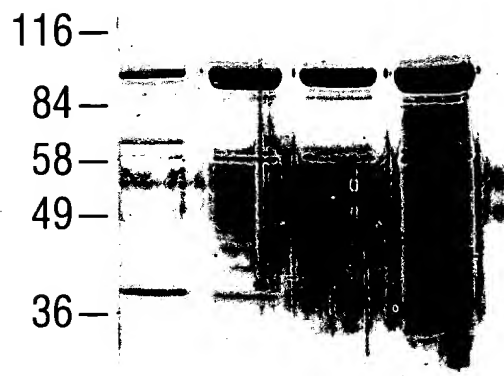


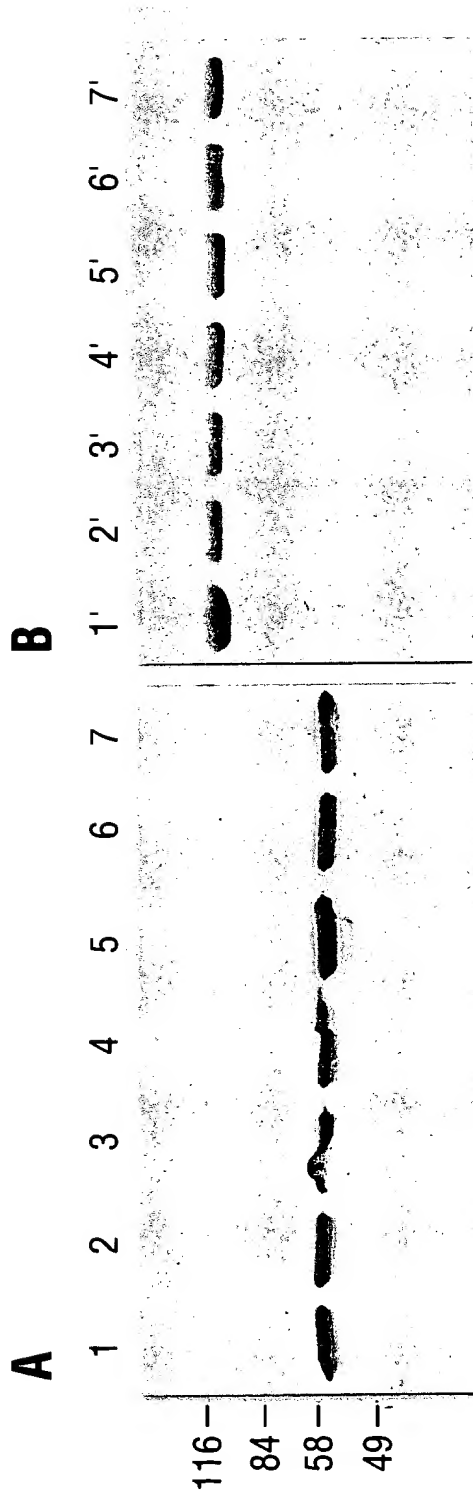
FIGURE 17C

i) h175

APPROVED	O. FIG.
CLASS	SUBCLASS



FIGURE 18B



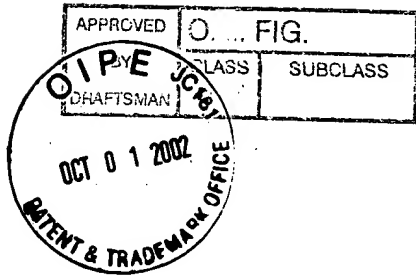


FIGURE 19A

HRP-bTf

h98

h99

h100

h105

h106

FIGURE 19B

Anti-Tbp1

FIGURE 19C

Anti-Tbp2

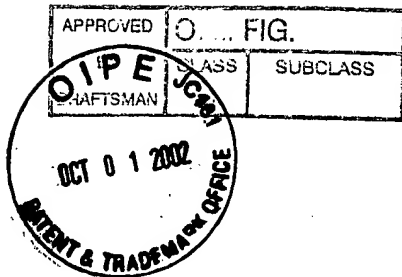
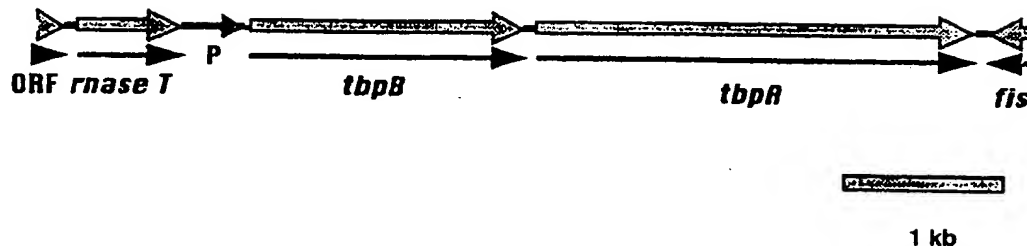


FIGURE 20A



1168
 ATTTTTTATCTAATCTAAAAACAAGCGTTTCCACCTTGGAATGATTAACATGATC
 CTGAAACTAATAAAGTTCAAACCTTTACATTAAGTTTATATTATAAATTATAATGA
 -35 -10
 TTATTATTTTATAAAATTAAAGGAGACATTATGTTTAAACTTAAAAGTAGTTTTGTA
 SD Met₁₃₀₉
 CTG.....*tbpB*.....GAAAAATAATCATAATCCCCTTTGCTGGTTGTAG
 SC₃₀₆₃
 ATAGCAAGCGGGCAATTTTTTTATAAAAATTTGCAAAATTTAAATAAAGGAGACCCT
 SD
 ATCTAATGATAATGAAATATCATCATTTTCGC.....*tbpA*.....AGAAA
 Met₃₁₅₁
 TTTCAGTTTAGCATTGAAATGAAGTTTGTAG.
 SC₅₉₄₃

FIGURE 20B

FIGURE 21

ATGATAATGAAATATCATCATTTTCGCTATTCACCTGTTGCCTTAACAGTGTATTGCTC
 TTTCTCATTCATACGGTGCTGCGACTGAAAATAAAAAAATCGAAGAAAATAACGATCTAGC
 TGTTCCTGGATGAAGTATTGTGACAGAGAGCCATTATGCTCACGAACGTCAAAACGAAGTA
 ACTGGCTTGGGGAAAGTAGTGAAAAATTATCACGAAATGAGTAAAAATCAAATTCCTTGGA
 TTCGTGATTTAACTCGCTATGACCCTGGTATTTTCGGTGGTGGAAACAAGGTCGCGGTGCAAG
 TAGTGGCTATGCCATTTCGAGGTGTAGATAAAAACCGTGTGCTAGCTTACTTGTGATGGGCTA
 CCACAAGCGCACAGTTATCATACGCTAGGTTTCAGATGCTAATGGTGGTGCAATTAATGAGA
 TTGAGTATGAAAACATTCGTTCAATTGAGTTAAGCAAAGGAGCAAGTTCGCGGAATATGG
 CTCTGGTGCGCATGGTGGTGCCTATTGGTTCGCTACTAAAGATGCGCAGGATATTATTAA
 GAGGGGCAGCATTGGGGCTTAGATAGTAAGACCTCTTATGCCAGCAAAAATAGCCATTTTT
 TACAGTCTATCGCAGCGGCTGGTGAGGCGGGTGGTTTTGAAGCACTTGTATTGCAACTCA
 CCGACACGGTAAAGAGACCAAAATTCATTCCGAGGCAAAATAAATTAACATAATATTCGG
 CGTATAACCGGCTTTGAAAATCGCTACGACTTTACCCAAATTCGCGACAGAATGCTCCTGG
 AGGATCTCCTTTTAATTGTGGAAGATACTTGCCCAACATTAGATTGTACTCCTCGTGCAAG
 GGTAAAGTTGAACCGCGATAATTTCCAGTGAGAACATTTCCGGAATATACGCCTGAAGAG
 CGCAAACAGCTTGAGCAGATTCCTTATCGCACTGAGCAGCTCTCAGCCCAAGAATATACCG
 GTAAAGATCGCATTGCACCAAACCCCTTTAGATTACAAGAGTAATTCGTTCCTTATGAAGTT
 TGGCTATCACTTCAACTCGTCTCATTATCTTGGCGCAATCTTAGAAGATACAAAACACGC
 TACGATATCCGTGATATGCAACGCCAGCTTACTATACAAAAGACGATATTAACCTTATCAC
 TTAGGAACCTATGTTTATGAAGGGGATAATATTTTAGATGGCTTAGTGTTCAGCCAAGGAT
 CCCTTATGGGTGCGCTATAGCCATGTGAAGTTTTTTTGATGAACGTCAACACAAACGTCGT
 TTAGGATTCACCTATAAATATAAACCAGAGAATAATCGCTGGTTGGATAGCATTAAACTCA
 GTGCGGATAAAACAAGATATTGAACTATATAGCCGGCTACATCGCTTGCAATTGTAGCGATTA
 TCCTGTGGTAGATAAAAATTGCCGCCGACTTTGGATAAATCTTGGTCTATGTATCGAACT
 GAGCGTAATAATTACCAAGAAAAGCATCGTGTCATTTAGAAATTTGATAAAGCGCTAA
 ATGCTGGTCAAGGCGTATTTAACCAAACCCACAACTGAATTTAGGGTTGGGCTTTGATCG
 ATTTAATTTCGCTTATGGATCATGGGGATATGACTGCCCAATATACCAAAGGCGGTTATACC
 AGCTACCGCGGTAGAGGGCGTTTAGATAATCCATATATTTATCGCCGCGATCCACGCAGTA
 TTGAAACGGTATCTTTGTGTAATAATACACGCGGCGACATCTTAACTGTGAACCGCGTAA
 AATTAAAGGCGATAGCCATTTTGTAGCTTCCGCGATCTAGTGATAAGCGAGTATGTGGAT
 TTGGGATTAGGGGTGCGTTTTGATCAACATCGATTTAAATCTGATGATCCGTGGACACTTA
 GCCGAACCTTATCGAAATTGGTCTTGGAAATGGTGGGATTACGCTTAAACCAACAGAGTTTGT
 ATCGCTTTCTTATCGCATTTCAAACGGTTTTAGAGTGCCTGCATTCTATGAACCTTTATGGT
 AAACGTGATCATATTGGGCTTAAAGATAACGAATATGTGCAACGCGCGCAACGTAGCCACC
 AGTTAGAGCCAGAAAAATCGACTAATCATGAGATTGGAGTTAGCTTTAAAGGTCAATTTGG
 TTACCTTGATGTGAGCTATTTCCGTAATAACTATAAAAAATATGATTGCGACAGCATGTAAA
 AGAATAATACAAAAATCACACTGTTTCTATAACTACCATAATATTCAAGATGTAGCACTAA
 ACGGGATAAATTTAGTCGCTAAATTTGACTTACACGGTATTTTATCTATGCTGCCAGATGG
 TTTTATTCATCAGTTGCTTATAACCGTGTAAGAGTAAAAGAGCGGAAACTAACCGACTCA
 AGACTCGATAGCGTAAACGATCCTATTCTAGATGCGATTCAGCCAGCACGCTATGTGCTTG
 GATTCGGCTACGATCACCCAGAAGAAAAATGGGAATTGGCATTACTACCCTATTCTTAA
 AGCCAAAACGCGGATGAGGTGGCAGGCACACGTCAACGNNATACATCCGCTTGATTAA
 GGTGGCAAACGTGACCGGTTCTTGGTACACCCATGATATTACCGGTTACATCAATTATAAAA
 ACTACACCTTACGTGGAGGAATTTATAATGTGACTAATCGTAAATATTCCACTTGGGAATC
 AGTGCGCCAATCCGGTGTGAATGCAGTAAACCAAGACCGGGGTAGCAATTACACTCGATTT
 GCGCTCCGGGGAGAAATTCAGTTTAGCATTTGAAATGAAGTTTTAG

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FIGURE 22

1 M I M K Y H H F R Y S P V A L T V L F A L S H S Y G A A T E
 31 N K K I E E N N D L A V L D E V I V T E S H Y A H E R O N E
 61 V T G L G K V V K N Y H E M S K N Q I L G I R D L T R Y D P
 91 G I S V Y E O G R G A S S G Y A I R G V D K N R V S L L V D
 121 G L P Q A H S Y H T L G S D A N G G A I N E I E Y E N I R S
 151 T E L S K G A S S A E Y G S G A H G G A I G F R T K D A Q D
 181 I I K E G Q H W G L D S K T S Y A S K N S H F L Q S I A A A
 211 G E A G G F E A L V I A T H R H G K E T K I H S E A N K L K
 241 H N I R R I T G F E N R Y D F T Q I P H R M L L E D L L L I
 271 V E D T C P T L D C T P R A R V K L N R D N F P V R T F P E
 301 Y T P E E R K Q L E Q I P Y R T E Q L S A Q E Y T G K D R I
 331 A P N P L D Y K S N S V F M K F G Y H F N S S H Y L G A I L
 361 E D T K T R Y D I R D M Q T P A Y Y T K D D I N L S L R N Y
 391 V Y E G D N I L D G L V F K P R I P Y G L R Y S H V K F F D
 421 E R H H K R R L G F T Y K Y K P E N N R W L D S I K L S A D
 451 K Q D I E L Y S R L H R L H C S D Y P V V D K N C R P T L D
 481 K S W S M Y R T E R N N Y Q E K H R V I H L E F D K A L N A
 511 G Q G V F N Q T H K L N L G L G F D R F N S L M D H G D M T
 541 A Q Y T K G G Y T S Y R G R G R L D N P Y I Y R R D P R S I
 571 E T V S L C N N T R G D I L N C E P R K I K G D S H F V S F
 601 R D L V I S E Y V D L G L G V R F D Q H R F K S D D P W T L
 631 S R T Y R N W S W N G G I T L K P T E F V S L S Y R I S N G
 661 F R V P A F Y E L Y G K R D H I G L K D N E Y V Q R A Q R S
 691 H Q L E P E K S T N H E I G V S F K G Q E G Y L D V S Y F R
 721 N N Y K N M I A T A C K R I I Q K S H C F Y N Y H N I Q D V
 751 A L N G I N L V A K F D L H G I L S M L P D G F Y S S V A Y
 781 N R V K Y K E R K L T D S R L D S V N D P I L D A I Q P A R
 811 Y V L G F G Y D H P E E K W G I G I T T T Y S K A K N A D E
 841 V A G T R H H G I H R V D L G G K L T G S W Y T H D I T G Y
 871 I N Y K N Y T L R G G I Y N V T N R K Y S T W E S Y R Q S G
 901 V N A V N Q D R G S N Y T R F G A P G R N F S L A F E M K E

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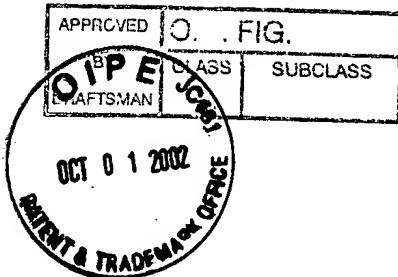


FIGURE 23

ATGTTTAAACTTAAAAGTAGTTTTGTACTGCTTAATGCGGCGCTACTTGCTGCTTGTTCCCT
CAAATGGTGGGAAGCTTTGATGTTCAATCTGCCAAAGTTGAATCTCAAACGCAAACCTACCCC
CAAAAAGCCAAGTTTACAAGATGATAATAGTAACGCAAGACGTACAGTAAGCGCTTCTGAA
ACTGAAGCTTTATTGTCAGCCGGGGTTTTGGTTTTTCAGCCAAAATTCGCGTCGTAATCTCC
TTCCGCAGGGGAAGGAAGATGTAGCCCCATTGGTGATATAAAAAGAGATTACTGGAGATCT
GCCAAAAATTCGTATGAAGAAGAGGTTAAAGCGTGCGGTAGTAGTGCTGATGGATTTAGC
CATACTCATGATAGAAATCATAAGTTGTATACAAGAGATTTTAATTTTGTTCGTTCCGGCT
ATGTTGTGCATTCTGGTCCAAAACCTGAAATAAAGCCTAAAGAAATTTTGAGAACAGGTGC
ACATGGGTATGTTTACTATTTAGGTATAGAGCCGCCCAAAGCAATACCTACCCAAAACTA
ACTTATAAAGGATATTGGGATTTTACTACCTATGCGGCTAAGGGGAGAGATAGTAATATTT
TTCTAATTCCCGCAGGCATCAATAGTGGCGCCATACCGGAAAATAGTCACGATATTAATGT
TGATGATTCTGAAAAACCAATGGGGCATAACAGGAGAATTTACGGCTGATTTTGCTAATAAA
ACTTTAACTGGAACATTGGTTCGTAATGGGTATGTTAGTCGTAGCAAAGAGCAAAAAATTA
CAACAATTTACGATATTGATGCGAAAATTAAGGTAATCGCTTTTCTGGTAAAGCAAACCC
AAAAAAACCGATGATCCTTATTTTTGGGAAAAGCTCCACGACACTTGAAGGTGGATTTTTT
GGTGGGGAGGCTCAAGAACTTGCCGGTAAATTCTTAGCTGATGATAAGTCGGTATTTGTTG
TTTTTGCTGGCACACGAGATGCTAAAAAGATGATAGTGAATCTGCCTTTGATGCTTTCCC
AATTAACTTAAAGATTTAAATAAATCTGAGATGGATACTTTCGGGAATGCGACACATTTG
ATTATTAACAATAAGCAGATTCCACTTATTGCGGAAGCCACAAAAGCTTTGCCGAGATGA
AATTTGATGATTTGGTTACCCGTACTATTGATGGAAAAACGTATCGAGTTTCAGTCTGCTG
TAATAATTTAGATTATGTCAAATTTGGGATTTATAGCGAGGGAAATAATAGTGATACTGCT
CTCCAAGAATATTTAGTAGGAGAACGTACAGCTCTGGCAGATTTGCCAACAGGGACAGTAA
AATATCGAGGTACTTGGGACGGGGTAATGTACAGTAAATCTGGCTCGGCAGGGGTTGAATC
GCCAAGTAACAGCGAAAGTGGTACTCGTTCACTATTCGATGTAGATTTTGTCAATAAAAAA
ATTAATGGCAAGCTGATTGCTAATGATGGTGTGAAGAACGCCAATGCTGACACTGGAAG
GCAATCTGAAAGGGAATGGTTTTGGAGGCACAGCCAAAACGGGCAATTCTGGTTTTAATCT
TGATCCCAAAGTACGAATGGTGGCACGGTAGGGCATATAAATACTCAATTTGAAGGGGGC
TTTTATGGCCCTAAGGCGACGGAATTAGGTGGTATTGTACAAAATACAGAAACGGATAAAG
ATAGAGTCAGTATTACATTCGGCGGAAAACGTCAAATAGAAAAATAA

FIGURE 24

1 MFKLLKSSFLNAA LLAACSSNGGSEEDVQS
 31 AKVESQTQTTPKKPSLODDNSNARRTVSAS
 61 ETEALLQPGFGFS AKIPRRNLLPQGKEDVA
 91 PIGDIKEITGDLPKIPYEEEVKACGSSADG
 121 FSHTHDRNHKLYTRDFN FVRS GYVVHSGPK
 151 PEIKPKEILRTGAH GYVY LGLIEPPKAIP T
 181 QK LTYKGYWDF TTYAAKGRDSNIFLIPAGI
 211 NSGAIPENSHDINVDDSEKPMGHT GEETAD
 241 FANKTLTGTLVRNG YVSR SKEQKITTIYDI
 271 DAKIKGNRES GKAN PKKPMILIFGKSSTTL
 301 EGGFFGGGEAQELAGKFLADDKSVFVVFAGT
 331 RDAKKDDSES AFDAFPIKLDL NKSEMDTF
 361 GNATHLIINN KQIPLIAEATKSFAEMKFDD
 391 LVTRTIDGKTYRVS VCCNNLDYVKFGIYSE
 421 GNNSDTALQE YLVGER TALADLPTGT VKYR
 451 GTWDG VMYSKSGSAGVESPSNSESGTRSL F
 481 DYDEVNKKINGKL IANDGVEERPMLTLEGN
 511 LKGN GEGGTAKTGN SGFNLDPKSTNGGTVG
 541 HINTQFE GGFYGPKATELGG IVQNTETDKD
 571 RV SITEGGKRQ IEK

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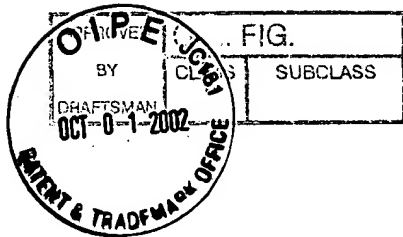


FIGURE 25

	HRP-bTf	HRP-oTf	HRP-gTf
h44 Fe +			
h44 Fe -			
h196			
h98			
h99			
h100			
h103			
h105			
h106			
h107			

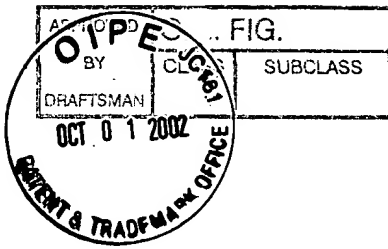


FIGURE 26A

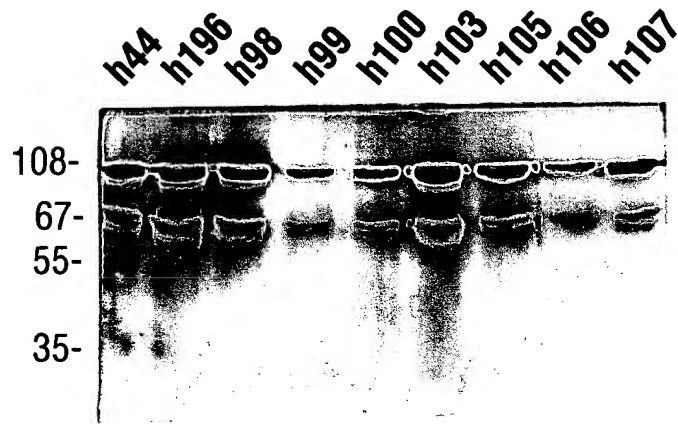
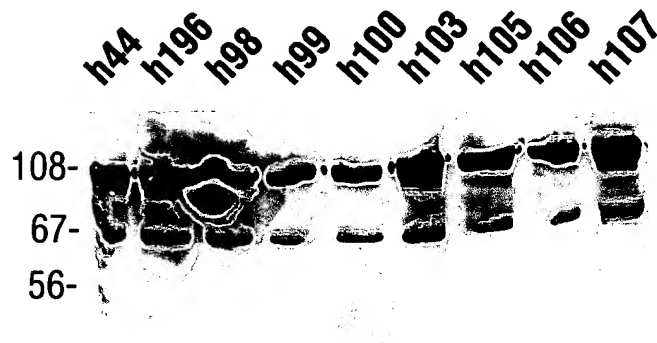


FIGURE 26B



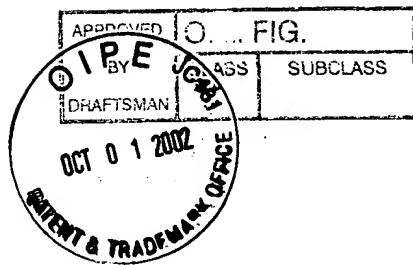


FIGURE 27

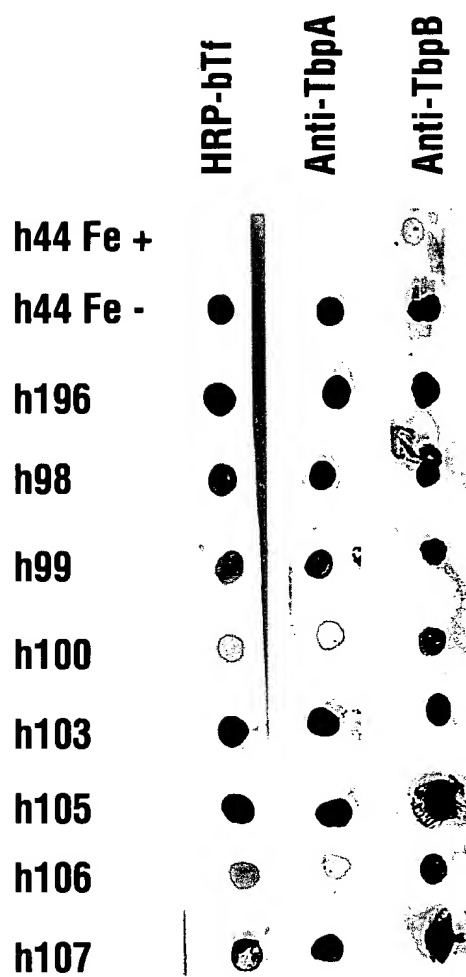


FIGURE 28A

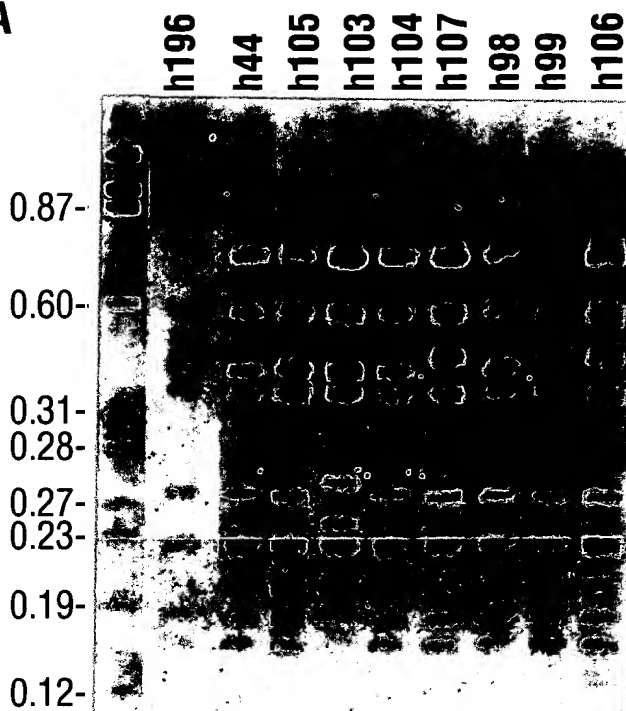
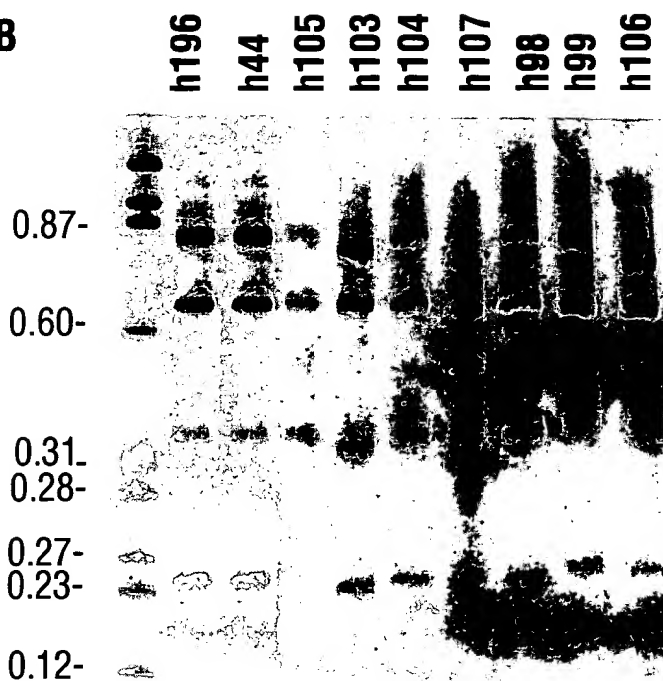


FIGURE 28B



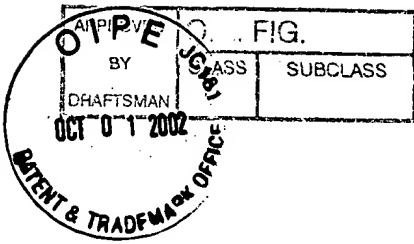


FIGURE 29A

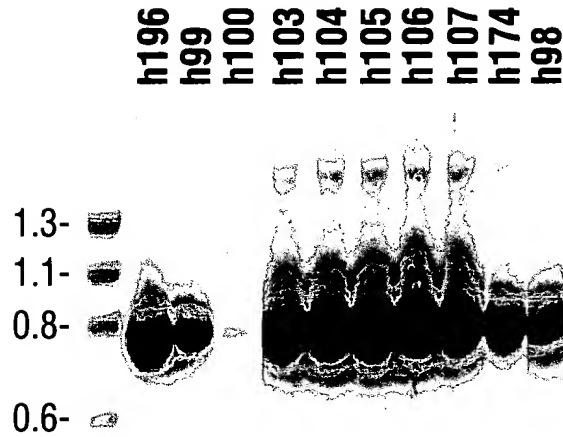


FIGURE 29B

